

Kazuho Ikeo

List of Publications by Year in descending order

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111
papers

6,767
citations

94433

37
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64796

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114
all docs

114
docs citations

114
times ranked

8100
citing authors

#	ARTICLE	IF	CITATIONS
1	Inhibition of BCL2A1 by STAT5 inactivation overcomes resistance to targeted therapies of FLT3-ITD/D835 mutant AML. <i>Translational Oncology</i> , 2022, 18, 101354.	3.7	9
2	Metatranscriptomic Analysis of Corals Inoculated With Tolerant and Non-Tolerant Symbiont Exposed to High Temperature and Light Stress. <i>Frontiers in Physiology</i> , 2022, 13, 806171.	2.8	3
3	<sc>TrBase</sc>: A genome and transcriptome database of <i>Temnopleurus reevesii</i>. <i>Development Growth and Differentiation</i> , 2022, 64, 210-218.	1.5	5
4	<sc>IFN</sc> mediated <sc>NK2R</sc> expression is related to the malignancy of colon cancer cells. <i>Cancer Science</i> , 2022, , .	3.9	7
5	DOCK11 and DENND2A play pivotal roles in the maintenance of hepatitis B virus in host cells. <i>PLoS ONE</i> , 2021, 16, e0246313.	2.5	8
6	Effects of Cordycepin in <i>Cordyceps militaris</i> during Its Infection to Silkworm Larvae. <i>Microorganisms</i> , 2021, 9, 681.	3.6	10
7	Development of a time-series shotgun metagenomics database for monitoring microbial communities at the Pacific coast of Japan. <i>Scientific Reports</i> , 2021, 11, 12222.	3.3	6
8	Diversity and functions of bacterial communities in water and sediment from the watershed of the Tama River flowing a highly urbanized area. <i>Fisheries Science</i> , 2021, 87, 697-715.	1.6	5
9	Multiple analysis of root exudates and microbiome in rice (<i>Oryza sativa</i>) under low P conditions. <i>Archives of Microbiology</i> , 2021, 203, 5599-5611.	2.2	7
10	Exogenous mitochondrial transfer and endogenous mitochondrial fission facilitate AML resistance to OxPhos inhibition. <i>Blood Advances</i> , 2021, 5, 4233-4255.	5.2	36
11	Metagenomic analysis provides functional insights into seasonal change of a non-cyanobacterial prokaryotic community in temperate coastal waters. <i>PLoS ONE</i> , 2021, 16, e0257862.	2.5	5
12	Usage of the Sea Urchin <i>Hemicentrotus pulcherrimus</i> Database, HpBase. <i>Methods in Molecular Biology</i> , 2021, 2219, 267-275.	0.9	0
13	Hydrophilic Shell Matrix Proteins of <i>Nautilus pompilius</i> and the Identification of a Core Set of Conchiferan Domains. <i>Genes</i> , 2021, 12, 1925.	2.4	7
14	Diverse Mechanisms of Resistance to Decitabine and Venetoclax Therapy in Newly Diagnosed and Relapsed/Refractory AML Inferred By Transcriptome Analysis. <i>Blood</i> , 2021, 138, 2244-2244.	1.4	2
15	Collagen adhesion gene is associated with bloodstream infections caused by methicillin-resistant <i>Staphylococcus aureus</i> . <i>International Journal of Infectious Diseases</i> , 2020, 91, 22-31.	3.3	8
16	Genomic and Transcriptomic Analyses of Bioluminescence Genes in the Enope Squid <i>Watasenia scintillans</i> . <i>Marine Biotechnology</i> , 2020, 22, 760-771.	2.4	3
17	Colour variation of the intertidal hermit crab <i>Clibanarius virescens</i> considering growth stage, geographic area in the Indo-West Pacific Ocean, and molecular phylogeny. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2020, 100, 1107-1121.	0.8	1
18	Establishment of homozygous knock-out sea urchins. <i>Current Biology</i> , 2020, 30, R427-R429.	3.9	24

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19	The increased frequency of methicillin-resistant <i>Staphylococcus aureus</i> with low MIC of beta-lactam antibiotics isolated from hospitalized patients. <i>Journal of Infection and Chemotherapy</i> , 2020, 26, 604-610.	1.7	5
20	The Scaly-foot Snail genome and implications for the origins of biomineralised armour. <i>Nature Communications</i> , 2020, 11, 1657.	12.8	64
21	BCL2A1: A Novel Target in Refractory Acute Myeloid Leukemia with FLT3-ITD/D835 Dual Mutations. <i>Blood</i> , 2020, 136, 32-33.	1.4	0
22	The Direct Interactions with Bone Marrow Microenvironment Confer Resistance to the Inhibition of Oxidative Phosphorylation in AML. <i>Blood</i> , 2020, 136, 11-11.	1.4	0
23	An Association Between Core Mutations in Hepatitis B Virus Genotype F1b and Hepatocellular Carcinoma in Alaskan Native People. <i>Hepatology</i> , 2019, 69, 19-33.	7.3	24
24	Aging of spermatogonial stem cells by Jnk-mediated glycolysis activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16404-16409.	7.1	39
25	Construction of complete <i>Tupaia belangeri</i> transcriptome database by whole-genome and comprehensive RNA sequencing. <i>Scientific Reports</i> , 2019, 9, 12372.	3.3	16
26	The reduction of miR146b-5p in monocytes and T cells could contribute to the immunopathogenesis of hepatitis C virus infection. <i>Scientific Reports</i> , 2019, 9, 13393.	3.3	5
27	Pirfenidone attenuates lung fibrotic fibroblast responses to transforming growth factor- β 1. <i>Respiratory Research</i> , 2019, 20, 119.	3.6	74
28	Clonal analysis revealed functional heterogeneity in cancer stem-like cell phenotypes in uterine endometrioid adenocarcinoma. <i>Experimental and Molecular Pathology</i> , 2019, 106, 78-88.	2.1	6
29	Specific Features of Fibrotic Lung Fibroblasts Highly Sensitive to Fibrotic Processes Mediated via TGF- β 1/ERK5 Interaction. <i>Cellular Physiology and Biochemistry</i> , 2019, 52, 822-837.	1.6	7
30	Cage Transcriptome Analysis Reveals BCL2A1 Upregulation in FLT3-ITD/D835 Dual Mutated AML Cells Harboring Complex Co-Mutations. <i>Blood</i> , 2019, 134, 1264-1264.	1.4	0
31	Oxphos Inhibition Induces Formation of Tunneling Nanotubes in AML Cells and Facilitates Mitochondrial Transfer from BM Stroma to AML That Contributes to Microenvironment-Mediated Drug-Resistance of AML. <i>Blood</i> , 2019, 134, 911-911.	1.4	11
32	HpBase: A genome database of a sea urchin, <i>Hemicentrotus pulcherrimus</i> . <i>Development Growth and Differentiation</i> , 2018, 60, 174-182.	1.5	39
33	Transcriptomic changes with increasing algal symbiont reveal the detailed process underlying establishment of coral-algal symbiosis. <i>Scientific Reports</i> , 2018, 8, 16802.	3.3	46
34	Maser: one-stop platform for NGS big data from analysis to visualization. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	42
35	Gene-by-gene or localized dosage compensation on the neo-X chromosome in <i>Drosophila miranda</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 1875-1881.	2.5	8
36	Molecular phylogeny of ten intertidal hermit crabs of the genus <i>Pagurus</i> inferred from multiple mitochondrial genes, with special emphasis on the evolutionary relationship of <i>Pagurus lanuginosus</i> and <i>Pagurus maculosus</i> . <i>Genetica</i> , 2018, 146, 369-381.	1.1	7

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37	Upregulation of Bcl-2 Confers Resistance to FLT3 Inhibition in FLT3-ITD AML with Secondary Acquired Mutations. <i>Blood</i> , 2018, 132, 3944-3944.	1.4	4
38	Combined Targeting of Bcl-2 and XPO1 Overcomes Acquired Resistance to Tyrosine Kinase Inhibitors in the FLT3-ITD/TKD Double Mutant AML. <i>Blood</i> , 2018, 132, 2640-2640.	1.4	1
39	Mitochondrial Transfer Confers Microenvironment-Mediated Resistance to Oxphos Inhibition in AML. <i>Blood</i> , 2018, 132, 430-430.	1.4	0
40	Bone Marrow Adipocytes Facilitate Fatty Acid Oxidation Activating AMPK and a Transcriptional Network Supporting Survival of Acute Monocytic Leukemia Cells. <i>Cancer Research</i> , 2017, 77, 1453-1464.	0.9	123
41	Genome-Wide Association Study Identifies TLL1 Variant Associated With Development of Hepatocellular Carcinoma After Eradication of Hepatitis C Virus Infection. <i>Gastroenterology</i> , 2017, 152, 1383-1394.	1.3	115
42	Constitutive centromere-associated network controls centromere drift in vertebrate cells. <i>Journal of Cell Biology</i> , 2017, 216, 101-113.	5.2	29
43	Comprehensive single-cell transcriptome analysis reveals heterogeneity in endometrioid adenocarcinoma tissues. <i>Scientific Reports</i> , 2017, 7, 14225.	3.3	23
44	Lack of interleukin-6 in the tumor microenvironment augments type-1 immunity and increases the efficacy of cancer immunotherapy. <i>Cancer Science</i> , 2017, 108, 1959-1966.	3.9	61
45	DNA Methylome Analysis Identifies Transcription Factor-Based Epigenomic Signatures of Multilineage Competence in Neural Stem/Progenitor Cells. <i>Cell Reports</i> , 2017, 20, 2992-3003.	6.4	45
46	Novel <i>C8orf37</i> Mutations in Patients with Early-onset Retinal Dystrophy, Macular Atrophy, Cataracts, and High Myopia. <i>Ophthalmic Genetics</i> , 2016, 37, 1-8.	1.2	17
47	Identification of Novel Mutations in the LRR-Cap Domain of <i>C21orf2</i> in Japanese Patients With Retinitis Pigmentosa and Cone-Rod Dystrophy. <i>Investigative Ophthalmology and Visual Science</i> , 2016, 57, 4255.		23
48	Accelerated pseudogenization on the neo-X chromosome in <i>Drosophila miranda</i> . <i>Nature Communications</i> , 2016, 7, 13659.	12.8	15
49	Effect of Wild and Cultivated Rice Genotypes on Rhizosphere Bacterial Community Composition. <i>Rice</i> , 2016, 9, 42.	4.0	75
50	Molecular Cloning of Secreted Luciferases from Marine Planktonic Copepods. <i>Methods in Molecular Biology</i> , 2016, 1461, 33-41.	0.9	0
51	Two-step evolution of endosymbiosis between hydra and algae. <i>Molecular Phylogenetics and Evolution</i> , 2016, 103, 19-25.	2.7	9
52	Acetylation of histone H4 lysine 5 and 12 is required for CENP-A deposition into centromeres. <i>Nature Communications</i> , 2016, 7, 13465.	12.8	66
53	CCT2 Mutations Evoke Leber Congenital Amaurosis due to Chaperone Complex Instability. <i>Scientific Reports</i> , 2016, 6, 33742.	3.3	27
54	VaProS: a database-integration approach for protein/genome information retrieval. <i>Journal of Structural and Functional Genomics</i> , 2016, 17, 69-81.	1.2	9

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55	Evolutionary Transitions of MicroRNA-Target Pairs. <i>Genome Biology and Evolution</i> , 2016, 8, 1621-1633.	2.5	23
56	Different Endosymbiotic Interactions in Two Hydra Species Reflect the Evolutionary History of Endosymbiosis. <i>Genome Biology and Evolution</i> , 2016, 8, 2155-2163.	2.5	24
57	<i>RPE65</i> Mutations in Two Japanese Families with Leber Congenital Amaurosis. <i>Ophthalmic Genetics</i> , 2016, 37, 161-169.	1.2	24
58	Genome-Wide Association Study Identifies ZNF354C Variants Associated with Depression from Interferon-Based Therapy for Chronic Hepatitis C. <i>PLoS ONE</i> , 2016, 11, e0164418.	2.5	9
59	Cap Analysis of Gene Expression (CAGE) Sequencing Reveals Alterations of the Transcriptional Signatures of FLT3-ITD with Secondary D835 TKD Mutations in Acute Myeloid Leukemia. <i>Blood</i> , 2016, 128, 1530-1530.	1.4	0
60	Comparative miRNAs analysis of Two contrasting broccoli inbred lines with divergent head-forming capacity under temperature stress. <i>BMC Genomics</i> , 2015, 16, 1026.	2.8	22
61	Function and Evolutionary Origin of Unicellular Camera-Type Eye Structure. <i>PLoS ONE</i> , 2015, 10, e0118415.	2.5	31
62	HJURP is involved in the expansion of centromeric chromatin. <i>Molecular Biology of the Cell</i> , 2015, 26, 2742-2754.	2.1	38
63	Cap Analysis of Gene Expression (CAGE) Sequencing Reveals Alterations of the Transcript Signatures in Acute Monocytic Leukemia Cells By Fatty Acid Oxidation Inhibition. <i>Blood</i> , 2015, 126, 3631-3631.	1.4	1
64	RHO Mutations (p.W126L and p.A346P) in Two Japanese Families with Autosomal Dominant Retinitis Pigmentosa. <i>Journal of Ophthalmology</i> , 2014, 2014, 1-10.	1.3	16
65	Coevolution of Axon Guidance Molecule Slit and Its Receptor Robo. <i>PLoS ONE</i> , 2014, 9, e94970.	2.5	7
66	Whole Exome Analysis Identifies Frequent CNGA1 Mutations in Japanese Population with Autosomal Recessive Retinitis Pigmentosa. <i>PLoS ONE</i> , 2014, 9, e108721.	2.5	56
67	Histone H4 Lys 20 Monomethylation of the CENP-A Nucleosome Is Essential for Kinetochores Assembly. <i>Developmental Cell</i> , 2014, 29, 740-749.	7.0	101
68	Gene dosage imbalance of human chromosome 21 in mouse embryonic stem cells differentiating to neurons. <i>Gene</i> , 2011, 481, 93-101.	2.2	6
69	The dynamic genome of Hydra. <i>Nature</i> , 2010, 464, 592-596.	27.8	743
70	Nematogalectin, a nematocyst protein with GlyXY and galectin domains, demonstrates nematocyte-specific alternative splicing in Hydra. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 18539-18544.	7.1	69
71	Biological Databases at DNA Data Bank of Japan in the Era of Next-Generation Sequencing Technologies. <i>Advances in Experimental Medicine and Biology</i> , 2010, 680, 125-135.	1.6	14
72	Genome Network Project: An Integrated Genomic Platform. <i>Nature Precedings</i> , 2009, , .	0.1	0

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73	DDBJ Activities: Contribution to the Research in Information Biology. Nature Precedings, 2009, , .	0.1	0
74	Eukaryotic nuclear structure explains the evolutionary rate difference of ribosome export factors. Gene, 2008, 421, 7-13.	2.2	1
75	The evolutionary relationship between gene duplication and alternative splicing. Gene, 2008, 427, 19-31.	2.2	34
76	Evola: Ortholog database of all human genes in H-InvDB with manual curation of phylogenetic trees. Nucleic Acids Research, 2007, 36, D787-D792.	14.5	33
77	The Rice Annotation Project Database (RAP-DB): 2008 update. Nucleic Acids Research, 2007, 36, D1028-D1033.	14.5	295
78	Curated genome annotation of <i>Oryza sativa</i> ssp. japonica and comparative genome analysis with <i>Arabidopsis thaliana</i> . Genome Research, 2007, 17, 175-183.	5.5	218
79	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. Nucleic Acids Research, 2007, 36, D793-D799.	14.5	57
80	Evolutionary origin of sex-related genes in the mouse brain. Gene, 2007, 406, 108-112.	2.2	1
81	Comparative genome analyses of nervous system-specific genes. Gene, 2006, 365, 130-136.	2.2	22
82	The Rice Annotation Project Database (RAP-DB): hub for <i>Oryza sativa</i> ssp. japonica genome information. Nucleic Acids Research, 2006, 34, D741-D744.	14.5	219
83	Evolutionary Process of Amino Acid Biosynthesis in <i>Corynebacterium</i> at the Whole Genome Level. Molecular Biology and Evolution, 2004, 21, 1683-1691.	8.9	26
84	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. PLoS Biology, 2004, 2, e162.	5.6	290
85	Comparative Analysis of Gene Expression for Convergent Evolution of Camera Eye Between Octopus and Human. Genome Research, 2004, 14, 1555-1561.	5.5	78
86	Detection of apoptosis during planarian regeneration by the expression of apoptosis-related genes and TUNEL assay. Gene, 2004, 333, 15-25.	2.2	92
87	The Human Anatomic Gene Expression Library (H-ANGEL), the H-Inv integrative display of human gene expression across disparate technologies and platforms. Nucleic Acids Research, 2004, 33, D567-D572.	14.5	16
88	Search for the Evolutionary Origin of a Brain: Planarian Brain Characterized by Microarray. Molecular Biology and Evolution, 2003, 20, 784-791.	8.9	73
89	Cloning and functional analysis of ascidian <i>Mitf</i> in vivo: insights into the origin of vertebrate pigment cells. Mechanisms of Development, 2003, 120, 1489-1504.	1.7	45
90	CIBEX: Center for Information Biology gene EXpression database. Comptes Rendus - Biologies, 2003, 326, 1079-1082.	0.2	138

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91	The genome stability in <i>Corynebacterium</i> species due to lack of the recombinational repair system. <i>Gene</i> , 2003, 317, 149-155.	2.2	66
92	Origin and evolutionary process of the CNS elucidated by comparative genomics analysis of planarian ESTs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 7666-7671.	7.1	172
93	Comparative Complete Genome Sequence Analysis of the Amino Acid Replacements Responsible for the Thermostability of <i>Corynebacterium efficiens</i> . <i>Genome Research</i> , 2003, 13, 1572-1579.	5.5	194
94	Induction of a noggin-Like Gene by Ectopic DV Interaction during Planarian Regeneration. <i>Developmental Biology</i> , 2002, 250, 59-70.	2.0	61
95	The expression of neural-specific genes reveals the structural and molecular complexity of the planarian central nervous system. <i>Mechanisms of Development</i> , 2002, 116, 199-204.	1.7	113
96	<i>HOX</i> genes in the sepiolid squid <i>Euprymna scolopes</i> : Implications for the evolution of complex body plans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 2088-2093.	7.1	60
97	Dissecting planarian central nervous system regeneration by the expression of neural-specific genes. <i>Development Growth and Differentiation</i> , 2002, 44, 135-146.	1.5	120
98	FGFR-related gene <i>nou-darake</i> restricts brain tissues to the head region of planarians. <i>Nature</i> , 2002, 419, 620-624.	27.8	244
99	Chinese spring wheat (<i>Triticum aestivum</i> L.) chloroplast genome: Complete sequence and contig clones. <i>Plant Molecular Biology Reporter</i> , 2000, 18, 243-253.	1.8	62
100	Pax 6: mastering eye morphogenesis and eye evolution. <i>Trends in Genetics</i> , 1999, 15, 371-377.	6.7	706
101	Structure and developmental expression of the ascidian TRP gene: Insights into the evolution of pigment cell-specific gene expression. <i>Developmental Dynamics</i> , 1999, 215, 225-237.	1.8	29
102	Mutation patterns for two flaviviruses: hepatitis C virus and GB virus C/hepatitis G virus. <i>FEBS Letters</i> , 1999, 450, 294-298.	2.8	0
103	Neural Network in Planarian Revealed by an Antibody against Planarian Synaptotagmin Homologue. <i>Biochemical and Biophysical Research Communications</i> , 1999, 260, 426-432.	2.1	68
104	Constrained evolution with respect to gene overlap of hepatitis B virus. <i>Journal of Molecular Evolution</i> , 1997, 44, S83-S90.	1.8	148
105	Ascidian tyrosinase gene: Its unique structure and expression in the developing brain. , 1997, 208, 363-374.		37
106	Ascidian tyrosinase gene: Its unique structure and expression in the developing brain. <i>Developmental Dynamics</i> , 1997, 208, 363-374.	1.8	4
107	Evolutionary relationship of hepatitis C, pesti-, flavi-, plantviruses, and newly discovered GB hepatitis agents. <i>FEBS Letters</i> , 1996, 378, 232-234.	2.8	93
108	Evolution of pathogenic viruses with special reference to the rates of synonymous and nonsynonymous substitutions.. <i>Japanese Journal of Genetics</i> , 1994, 69, 481-488.	1.0	28

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109	Cloning of human, mouse and fission yeast recombination genes homologous to RAD51 and recA. Nature Genetics, 1993, 4, 239-243.	21.4	506
110	Evolutionary origin of numerous kringles in human and simian apolipoprotein(a). FEBS Letters, 1991, 287, 146-148.	2.8	21
111	Mutation pattern of human immunodeficiency virus genes. Journal of Molecular Evolution, 1991, 32, 360-363.	1.8	32